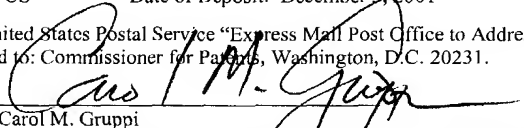


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Carol M. Gruppi

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Inventor: Malcolm J. Simons

Assignee:

GeneType A.G.

Serial No.: To Be Assigned

Examiner:

To Be Assigned

Filing Date: December 3, 2001

Group Art Unit:

To Be Assigned

For: Intron Sequence Analysis Method For Detection Of Adjacent And Remote Locus Alleles
As Haplotypes

PRELIMINARY AMENDMENT PURSUANT TO 37 C.F.R. § 1.115

Commissioner for Patents
BOX PATENT APPLICATION
Washington, D.C. 20231

Sir:

Prior to examination of the above-identified application, please amend the application as indicated below.

IN THE SPECIFICATION

At page 1, line 2, after "is," insert --a Continuation of U.S. application Serial No. 09/070,497 filed October 16, 2000 which is a continued prosecution application of application Serial No. 09/070,497, filed April 30, 1998, a Continuation of U.S. application Serial No. 08/682,054, filed July 16, 1996, which is a Divisional of U.S. application Serial No. 07/949,652, filed September 23, 1992 (now U.S. Patent No. 5,612,179) which is a Continuation of U.S. application Serial No. 07/551,239, filed July 11, 1990 (now U.S. Patent No. 5,192,659), which is --

IN THE CLAIMS

Please cancel Claims 1-34 without prejudice, and add the following claims.

1. A method for characterizing a coding region allele or haplotype of a multi-allelic genetic locus comprising:
 - (a) selecting a region of genomic DNA comprising a non-coding region sequence in genetic linkage with said genetic locus, wherein said non-coding region sequence comprises one or more genetic variations characteristic of a coding-region allele or haplotype or a group of coding-region alleles or haplotypes; and
 - (b) identifying said one or more genetic variations in a genomic DNA sample to identify said coding-region allele or haplotype or group of coding-region alleles or haplotypes.
2. The method of Claim 2 additionally comprising:
 - (a) selecting a region of genomic DNA comprising a coding region sequence, wherein said coding region sequence comprises one or more genetic variations characteristic of a coding-region allele or haplotype or a group of coding-region alleles or haplotypes; and
 - (b) identifying said one or more genetic variations in said coding region in a genomic DNA sample to identify said coding-region allele or haplotype or group of coding-region alleles or haplotypes.
3. The method of Claim 2 wherein the identification of a combination of genetic variations in said coding and non-coding region sequences allows the identification of a coding region allele or haplotype.

REMARKS

Claims 1-34 have been canceled, and Claims 1-3 have been added. Therefore, Claims 1-3 are pending in the application.

Support for the amendments is as follows. Support for Claim 1 is found in the specification at least at page 7, lines 33-36; page 8, line 16-22; page 10, lines 5-8 and lines 14-36; page 14, lines 10-14; and page 89, lines 305. Claim 2 finds support at least at page 15, lines 21-25, taken with page 17, lines 13-16. Support for Claim 3 is found at least at page 14, lines 10-14. No new matter is added by any of the amendments. A copy of the claims pending after the amendment is attached hereto as Exhibit A.

Conditional Petition for Extension of Time: An extension of time is requested to provide for timely filing if an extension of time is still required after all papers filed with this communication have been considered.

If a telephone conference would expedite the prosecution of this application, the Examiner is requested to telephone and confer with the undersigned attorney.

Dated: December 3, 2001

Respectfully submitted,

By: _____

Carol M. Gruppi

Registration No.: 37,341

McCutchen, Doyle, Brown & Enersen, LLP
Three Embarcadero Center, Suite 1800
San Francisco, California 94111
Telephone: (650) 849-4902
Fax: (650) 849-4800

EXHIBIT A
CURRENTLY PENDING CLAIMS

11046 U.S. PTO
10/005626
12/03/01

1. A method for characterizing a coding region allele or haplotype of a multi-allelic genetic locus comprising:

- (a) selecting a region of genomic DNA comprising a non-coding region sequence in genetic linkage with said genetic locus, wherein said non-coding region sequence comprises one or more genetic variations characteristic of a coding-region allele or haplotype or a group of coding-region alleles or haplotypes; and
- (b) identifying said one or more genetic variations in a genomic DNA sample to identify said coding-region allele or haplotype or group of coding-region alleles or haplotypes.

2. The method of Claim 2 additionally comprising:

- (a) selecting a region of genomic DNA comprising a coding region sequence, wherein said coding region sequence comprises one or more genetic variations characteristic of a coding-region allele or haplotype or a group of coding-region alleles or haplotypes; and
- (b) identifying said one or more genetic variations in said coding region in a genomic DNA sample to identify said coding-region allele or haplotype or group of coding-region alleles or haplotypes.

3. The method of Claim 2 wherein the identification of a combination of genetic variations in said coding and non-coding region sequences allows the identification of a coding region allele or haplotype.

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